

## Appendix B

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## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment.

The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program ☒ blastp ☒ Matrix ☐ Not Applicable ☒

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch: ☐ Use Mega BLAST Strand option ☐ Both strands ☒Open gap  and extension gap  penalties  
gap x\_dropoff  expect  word size  Filter ☒ Align Sequence 1 Enter accession or GI  or download from file   
or sequence in FASTA format from:  to: 

LXXXXXXXXXXEVLKEXQALQTVCL

Sequence 2 Enter accession or GI  or download from file   
or sequence in FASTA format from:  to:

VASLRQQVEALQGQVQHLQAAFSQYKK

Align

Clear Input

*Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)*

**Blast 2 Sequences results**

PubMed Entrez BLAST OMIM Taxonomy Structure

**BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]**Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.0000** wordsize: **3** Filter ☒ Align

Sequence 1 lc|seq\_1 Length 26

Sequence 2 lc|seq\_2 Length 27

No significant similarity was found

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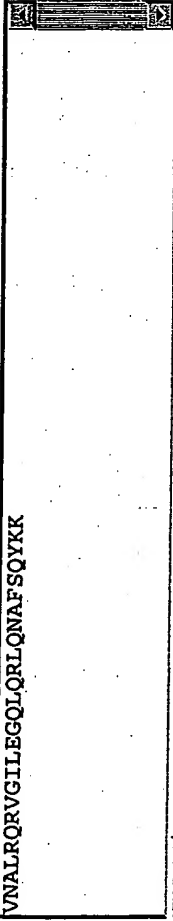
## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using [BLAST](#) engine for local alignment. The stand-alone executable for blasting two sequences (b12seq) can be retrieved from [NCBI ftp site](#).  
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program ☒ [blastp](#) ☒ [Matrix](#) ☐ [Not Applicable](#)Parameters used in [BLASTN](#) program only:Reward for a match:  Penalty for a mismatch: ☐ Use [Mega BLAST](#) Strand option ☒ Both strandsOpen gap  and extension gap  penalties  
gap x\_dropoff  expect  word size  Filter ☒ [Align](#)Sequence 1 Enter accession or GI  or download from file  [Browse](#)  
or sequence in FASTA format from:  to: LXXXXXXXXXXEYXLLKEXQALQTVCLSequence 2 Enter accession or GI  or download from file  [Browse](#)  
or sequence in FASTA format from:  to: 

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VNALRQRVGILEGQLQRLQNAFSQYKK



Align Clear Input

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**Blast 2 Sequences results**

PubMed Entrez BLAST OMIM Taxonomy Structure

**BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]**Matrix **BLOSUM62** gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter ☒ Align

Sequence 1 lc|seq\_1 Length 26

Sequence 2 lc|seq\_2 Length 27

No significant similarity was found

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Program ☒ blastp ☒ Matrix ☐ Not Applicable ☒Parameters used in BLASTN program only:Reward for a match:  Penalty for a mismatch: ☐ Use Mega BLAST Strand option ☐ Both strands ☒Open gap  and extension gap  penalties  
gap x\_dropoff  expect  word size  Filter ☒ Align Sequence 1 Enter accession or GI  or download from file   
or sequence in FASTA format from:  to Sequence 2 Enter accession or GI  or download from file   
or sequence in FASTA format from:  to 

C 1/3



SAALROQMEALNGKLQRLEAAF SRYKK

Align Clear Input

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**Blast 2 Sequences results**

PubMed Entrez BLAST OMIM Taxonomy Structure

**BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]**

Matrix **BLOSUM62** gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter ☒ Align

Sequence 1 lc|seq\_1 Length 26

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Program ☒ blastp ☒ Matrix ☒ Not Applicable ☒

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch:

☐ Use Mega BLAST Strand option ☒ Both strands ☒

Open gap  and extension gap  penalties  
gap x\_dropoff  expect  word size  Filter ☒ Align

Sequence 1 Enter accession or GI  or download from file   
or sequence in FASTA format from:  to:

LXXXXXXXXXXEVXXLKEXQALQTVCL

Sequence 2 Enter accession or GI  or download from file   
or sequence in FASTA format from:  to:

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VNALKQRTVLTLDGHLRRFQNAFSQYKK

Align Clear Input

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)

D2/3

**Blast 2 Sequences results**

PubMed Entrez BLAST OMIM Taxonomy Structure

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x\_dropoff: **50** expect: **10.0000** wordsize: **3** Filter ☒ Align

Sequence 1 lc|seq\_1 Length 26

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## BLAST 2 SEQUENCES

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Program ☒ blastp ☒ Matrix ☐ Not Applicable ☒Parameters used in BLASTN program only:Reward for a match:  Penalty for a mismatch: ☐ Use Mega BLAST Strand option ☒ Both strands ☒Open gap  and extension gap  penaltiesgap x\_dropoff  expect  word size  Filter ☒ Align Sequence 1 Enter accession or GI  or download from file or sequence in FASTA format from:  to: Sequence 2 Enter accession or GI  or download from file or sequence in FASTA format from:  to: 

E 1/3

VDTLRQRMNLEGEVQRIQNIVTQYRK

Align Clear Input

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)

E 2/3

**Blast 2 Sequences results**

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**BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]**

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